

10/539956

**RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/539,956

Source: PCT

Date Processed by STIC: 06-30-05

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PCT

## RAW SEQUENCE LISTING

DATE: 06/30/2005

PATENT APPLICATION: US/10/539,956

TIME: 09:32:25

Input Set : E:\UTSH264US.txt

Output Set: N:\CRF4\06302005\J539956.raw

3 <110> APPLICANT: NORRIS, STEVEN J.

5 <120> TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA SPECIES AND STRAINS

7 <130> FILE REFERENCE: UTSH:264US

C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,956

10 <141> CURRENT FILING DATE: 2005-06-17

12 <150> PRIOR APPLICATION NUMBER: PCT/US2003/04118

13 <151> PRIOR FILING DATE: 2003-12-22

15 <150> PRIOR APPLICATION NUMBER: 60/435,077

16 <151> PRIOR FILING DATE: 2002-12-20

18 <160> NUMBER OF SEQ ID NOS: 81

20 <170> SOFTWARE: PatentIn Ver. 2.1

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 1227

24 <212> TYPE: DNA

25 <213> ORGANISM: Borrelia burgdorferi

27 <220> FEATURE:

28 <221> NAME/KEY: CDS

29 <222> LOCATION: (75)..(1142)

31 <400> SEQUENCE: 1

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34 aggagacgat gaat atg aaa aaa att tca agt gca agt tta tta aca act 110

35 Met Lys Lys Ile Ser Ser Ala Ser Leu Leu Thr Thr

36 1 5 10

38 ttc ttt gtt ttt att aat tgt aaa agc caa gtt gct gat aag gac gac 158

39 Phe Phe Val Phe Ile Asn Cys Lys Ser Gln Val Ala Asp Lys Asp Asp

40 15 20 25

42 cca aca aac aaa ttt tac caa tct gtc ata caa tta ggt aac gga ttt 206

43 Pro Thr Asn Lys Phe Tyr Gln Ser Val Ile Gln Leu Gly Asn Gly Phe

44 30 35 40

46 ctt gat gta ttc aca tct ttt ggt ggg tta gta gca gag gct ttt gga 254

47 Leu Asp Val Phe Thr Ser Phe Gly Gly Leu Val Ala Glu Ala Phe Gly

48 45 50 55 60

50 ttt aaa tca gat cca aaa aaa tct gat gta aaa acc tat ttt act act 302

51 Phe Lys Ser Asp Pro Lys Lys Ser Asp Val Lys Thr Tyr Phe Thr Thr

52 65 70 75

54 gta gct gcc aaa ttg gaa aaa aca aaa acc gat ctt aat agt ttg cct 350

55 Val Ala Ala Lys Leu Glu Lys Thr Lys Thr Asp Leu Asn Ser Leu Pro

56 80 85 90

58 aag gaa aaa agc gat ata agt agt acg acg ggg aaa cca gat agt aca 398

59 Lys Glu Lys Ser Asp Ile Ser Ser Thr Thr Gly Lys Pro Asp Ser Thr

60 95 100 105

62 ggt tct gtt gga act gcc gtt gag ggg gct att aag gaa gtt agc gag 446

63 Gly Ser Val Gly Thr Ala Val Glu Gly Ala Ile Lys Glu Val Ser Glu

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64      110      115      120
66 ttg ttg gat aag ctg gta aaa gct gta aag aca gct gag ggg gct tca 494
67 Leu Leu Asp Lys Leu Val Lys Ala Val Lys Thr Ala Glu Gly Ala Ser
68 125      130      135      140
70 agt ggt act gct gca att gga gaa gtt gtg gct gat gct gat gct gca 542
71 Ser Gly Thr Ala Ala Ile Gly Glu Val Val Ala Asp Ala Asp Ala Ala
72      145      150      155
74 aag gtt gct gat aag gcg agt gtg aag ggg att gct aag ggg ata aag 590
75 Lys Val Ala Asp Lys Ala Ser Val Lys Gly Ile Ala Lys Gly Ile Lys
76      160      165      170
78 gag att gtt gaa gct gct ggg ggg agt gaa aag ctg aaa gct gtt gct 638
79 Glu Ile Val Glu Ala Ala Gly Gly Ser Glu Lys Leu Lys Ala Val Ala
80      175      180      185
82 gct gct aaa ggg gag aat aat aaa ggg gca ggg aag ttg ttt ggg aag 686
83 Ala Ala Lys Gly Glu Asn Asn Lys Gly Ala Gly Lys Leu Phe Gly Lys
84      190      195      200
86 gct ggt gct gct gct cat ggg gac agt gag gct gct agc aag gcg gct 734
87 Ala Gly Ala Ala Ala His Gly Asp Ser Glu Ala Ala Ser Lys Ala Ala
88 205      210      215      220
90 ggt gct gtt agt gct gtt agt ggg gag cag ata tta agt gcg att gtt 782
91 Gly Ala Val Ser Ala Val Ser Gly Glu Gln Ile Leu Ser Ala Ile Val
92      225      230      235
94 acg gct gct gat gcg gct gag cag gat gga aag aag cct gag gag gct 830
95 Thr Ala Ala Asp Ala Ala Glu Gln Asp Gly Lys Lys Pro Glu Glu Ala
96      240      245      250
98 aaa aat ccg att gct gct gct att ggg gat aaa gat ggg ggt gcg gag 878
99 Lys Asn Pro Ile Ala Ala Ala Ile Gly Asp Lys Asp Gly Gly Ala Glu
100      255      260      265
102 ttt ggt cag gat gag atg aag aag gat gat cag att gct gct gct att 926
103 Phe Gly Gln Asp Glu Met Lys Lys Asp Asp Gln Ile Ala Ala Ala Ile
104      270      275      280
106 gct ttg agg ggg atg gct aag gat gga aag ttt gct gtg aag gat ggt 974
107 Ala Leu Arg Gly Met Ala Lys Asp Gly Lys Phe Ala Val Lys Asp Gly
108 285      290      295      300
110 gag aaa gag aag gct gag ggg gct att aag gga gct gct gag tct gca 1022
111 Glu Lys Glu Lys Ala Glu Gly Ala Ile Lys Gly Ala Ala Glu Ser Ala
112      305      310      315
114 gtt cgc aaa gtt tta ggg gct att act ggg cta ata gga gac gcc gtg 1070
115 Val Arg Lys Val Leu Gly Ala Ile Thr Gly Leu Ile Gly Asp Ala Val
116      320      325      330
118 agt tcc ggg cta agg aaa gtc ggt gat tca gtg aag gct gct agt aaa 1118
119 Ser Ser Gly Leu Arg Lys Val Gly Asp Ser Val Lys Ala Ala Ser Lys
120      335      340      345
122 gaa aca cct cct gcc ttg aat aag tgatttaatt aagtgtatgg acacgactat 1172
123 Glu Thr Pro Pro Ala Leu Asn Lys
124      350      355
126 gccctcatga ttgaggaaat agtcgagaga tatatatatact aaaagataat aaata 1227
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 356

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131 <212> TYPE: PRT
132 <213> ORGANISM: Borrelia burgdorferi
134 <400> SEQUENCE: 2
135 Met Lys Lys Ile Ser Ser Ala Ser Leu Leu Thr Thr Phe Phe Val Phe
136 1 5 10 15
138 Ile Asn Cys Lys Ser Gln Val Ala Asp Lys Asp Asp Pro Thr Asn Lys
139 20 25 30
141 Phe Tyr Gln Ser Val Ile Gln Leu Gly Asn Gly Phe Leu Asp Val Phe
142 35 40 45
144 Thr Ser Phe Gly Gly Leu Val Ala Glu Ala Phe Gly Phe Lys Ser Asp
145 50 55 60
147 Pro Lys Lys Ser Asp Val Lys Thr Tyr Phe Thr Thr Val Ala Ala Lys
148 65 70 75 80
150 Leu Glu Lys Thr Lys Thr Asp Leu Asn Ser Leu Pro Lys Glu Lys Ser
151 85 90 95
153 Asp Ile Ser Ser Thr Thr Gly Lys Pro Asp Ser Thr Gly Ser Val Gly
154 100 105 110
156 Thr Ala Val Glu Gly Ala Ile Lys Glu Val Ser Glu Leu Leu Asp Lys
157 115 120 125
159 Leu Val Lys Ala Val Lys Thr Ala Glu Gly Ala Ser Ser Gly Thr Ala
160 130 135 140
162 Ala Ile Gly Glu Val Val Ala Asp Ala Asp Ala Lys Val Ala Asp
163 145 150 155 160
165 Lys Ala Ser Val Lys Gly Ile Ala Lys Gly Ile Lys Glu Ile Val Glu
166 165 170 175
168 Ala Ala Gly Gly Ser Glu Lys Leu Lys Ala Val Ala Ala Ala Lys Gly
169 180 185 190
171 Glu Asn Asn Lys Gly Ala Gly Lys Leu Phe Gly Lys Ala Gly Ala Ala
172 195 200 205
174 Ala His Gly Asp Ser Glu Ala Ala Ser Lys Ala Ala Gly Ala Val Ser
175 210 215 220
177 Ala Val Ser Gly Glu Gln Ile Leu Ser Ala Ile Val Thr Ala Ala Asp
178 225 230 235 240
180 Ala Ala Glu Gln Asp Gly Lys Lys Pro Glu Glu Ala Lys Asn Pro Ile
181 245 250 255
183 Ala Ala Ala Ile Gly Asp Lys Asp Gly Gly Ala Glu Phe Gly Gln Asp
184 260 265 270
186 Glu Met Lys Lys Asp Asp Gln Ile Ala Ala Ala Ile Ala Leu Arg Gly
187 275 280 285
189 Met Ala Lys Asp Gly Lys Phe Ala Val Lys Asp Gly Glu Lys Glu Lys
190 290 295 300
192 Ala Glu Gly Ala Ile Lys Gly Ala Ala Glu Ser Ala Val Arg Lys Val
193 305 310 315 320
195 Leu Gly Ala Ile Thr Gly Leu Ile Gly Asp Ala Val Ser Ser Gly Leu
196 325 330 335
198 Arg Lys Val Gly Asp Ser Val Lys Ala Ala Ser Lys Glu Thr Pro Pro
199 340 345 350
201 Ala Leu Asn Lys
202 355

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206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1141
208 <212> TYPE: DNA
209 <213> ORGANISM: Borrelia hermsii
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (1)..(1062)
215 <400> SEQUENCE: 3
216 atg aga aaa aga ata agt gca ata ata atg act tta ttt atg gta tta 48
217 Met Arg Lys Arg Ile Ser Ala Ile Ile Met Thr Leu Phe Met Val Leu
218 1 5 10 15
220 gta agc tgt aat agc ggt ggg gtt gcg gaa gat cct aaa act gtg tat 96
221 Val Ser Cys Asn Ser Gly Gly Val Ala Glu Asp Pro Lys Thr Val Tyr
222 20 25 30
224 tta aca tct ata gct aat tta ggg aaa gga ttt tta gat gtt ttt gtg 144
225 Leu Thr Ser Ile Ala Asn Leu Gly Lys Gly Phe Leu Asp Val Phe Val
226 35 40 45
228 act ttt gga gat atg gtt act gga gct ttt ggt att aag gca gat act 192
229 Thr Phe Gly Asp Met Val Thr Gly Ala Phe Gly Ile Lys Ala Asp Thr
230 50 55 60
232 aag aaa agt gat ata ggg aag tat ttt act gat att gag agc act atg 240
233 Lys Lys Ser Asp Ile Gly Lys Tyr Phe Thr Asp Ile Glu Ser Thr Met
234 65 70 75 80
236 aca tca gtt aaa aag aag ttg caa gat gaa gtt gct aag aat ggt aac 288
237 Thr Ser Val Lys Lys Lys Leu Gln Asp Glu Val Ala Lys Asn Gly Asn
238 85 90 95
240 tat cca aag gta aag aca gct gtt gac gaa ttt gtt gca atc tta gga 336
241 Tyr Pro Lys Val Lys Thr Ala Val Asp Glu Phe Val Ala Ile Leu Gly
242 100 105 110
244 aag atc gag aaa gga gca aaa gaa gca tct aaa ggg gct act ggt gat 384
245 Lys Ile Glu Lys Gly Ala Lys Glu Ala Ser Lys Gly Ala Thr Gly Asp
246 115 120 125
248 gtt att att ggg aat act gtt aag aat ggt gat gct gta cct gga gaa 432
249 Val Ile Ile Gly Asn Thr Val Lys Asn Gly Asp Ala Val Pro Gly Glu
250 130 135 140
252 gca aca agt gtc aat tct ctt gtt aaa gga att aaa gaa ata gtt ggg 480
253 Ala Thr Ser Val Asn Ser Leu Val Lys Gly Ile Lys Glu Ile Val Gly
254 145 150 155 160
256 gta gtc ttg aag gaa ggt aag gca gat gct gat gct act aaa gat gat 528
257 Val Val Leu Lys Gly Lys Ala Asp Ala Asp Ala Thr Lys Asp Asp
258 165 170 175
260 agt aag aaa gat att ggt aaa tta ttt acc gca acc act gat gcg aat 576
261 Ser Lys Lys Asp Ile Gly Lys Leu Phe Thr Ala Thr Thr Asp Ala Asn
262 180 185 190
264 aga gct gat aat gcg gca gct caa gca gct gca gcg tca ata gga gca 624
265 Arg Ala Asp Asn Ala Ala Ala Gln Ala Ala Ala Ser Ile Gly Ala
266 195 200 205
268 gtg aca ggt gct gat atc ttg caa gct ata gta caa tct aag gaa aat 672
269 Val Thr Gly Ala Asp Ile Leu Gln Ala Ile Val Gln Ser Lys Glu Asn

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270      210      215      220
272 cct gtt gca aat agt act gat gga att gaa aaa gca aca gat gca gct 720
273 Pro Val Ala Asn Ser Thr Asp Gly Ile Glu Lys Ala Thr Asp Ala Ala
274 225      230      235      240
276 gag att gca gtt gct cca gct aaa gat aat aaa aaa gag att aaa gat 768
277 Glu Ile Ala Val Ala Pro Ala Lys Asp Asn Lys Lys Glu Ile Lys Asp
278      245      250      255
280 gga gca aaa aaa gac gca gtt att gct gca ggc att gca ctg cga gca 816
281 Gly Ala Lys Lys Asp Ala Val Ile Ala Ala Gly Ile Ala Leu Arg Ala
282      260      265      270
284 atg gct aag aat ggt aca ttt tct att aaa aac aat gaa gat gcg gct 864
285 Met Ala Lys Asn Gly Thr Phe Ser Ile Lys Asn Asn Glu Asp Ala Ala
286      275      280      285
288 gta acg acg ata aat agt gca gca gca agc gca gtg aac aag att tta 912
289 Val Thr Thr Ile Asn Ser Ala Ala Ala Ser Ala Val Asn Lys Ile Leu
290      290      295      300
292 agc act cta ata ata gca ata agg aat aca gtt gat agt ggt tta aaa 960
293 Ser Thr Leu Ile Ile Ala Ile Arg Asn Thr Val Asp Ser Gly Leu Lys
294 305      310      315      320
296 aca ata aat gag gct ctt gct aca gtt aaa caa gaa gat aaa tct gta 1008
297 Thr Ile Asn Glu Ala Leu Ala Thr Val Lys Gln Glu Asp Lys Ser Val
298      325      330      335
300 gaa gca act aat act gca gaa gca aca act agt ggt cag caa gcg aaa 1056
301 Glu Ala Thr Asn Thr Ala Glu Ala Thr Thr Ser Gly Gln Gln Ala Lys
302      340      345      350
304 aac tag ttaagggttaa atataaagga taaagttatt gtaagggaaa agcttttctt 1112
305 Asn
307 gtttttaatg caggaatgta gtttctctg 1141
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 353
312 <212> TYPE: PRT
313 <213> ORGANISM: Borrelia hermsii
315 <400> SEQUENCE: 4
316 Met Arg Lys Arg Ile Ser Ala Ile Ile Met Thr Leu Phe Met Val Leu
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318 Val Ser Cys Asn Ser Gly Gly Val Ala Glu Asp Pro Lys Thr Val Tyr
319      20      25      30
320 Leu Thr Ser Ile Ala Asn Leu Gly Lys Gly Phe Leu Asp Val Phe Val
321      35      40      45
322 Thr Phe Gly Asp Met Val Thr Gly Ala Phe Gly Ile Lys Ala Asp Thr
323      50      55      60
324 Lys Lys Ser Asp Ile Gly Lys Tyr Phe Thr Asp Ile Glu Ser Thr Met
325      65      70      75      80
326 Thr Ser Val Lys Lys Lys Leu Gln Asp Glu Val Ala Lys Asn Gly Asn
327      85      90      95
328 Tyr Pro Lys Val Lys Thr Ala Val Asp Glu Phe Val Ala Ile Leu Gly
329      100      105      110
330 Lys Ile Glu Lys Gly Ala Lys Glu Ala Ser Lys Gly Ala Thr Gly Asp
331      115      120      125

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/539,956

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TIME: 09:32:26

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number